

scFv(UCHT-1)-PE38

single chain Fv fragment

# amino acid
residues:

109 16 122 5

347

VL=light chain variable region

L = peptide linker (GGGS)₄

VH=heavy chain variable region

C = connector segment (KASGG)

Toxin = PE38 fragment of *Pseudomonas aeruginosa* exotoxin A

FIG.1

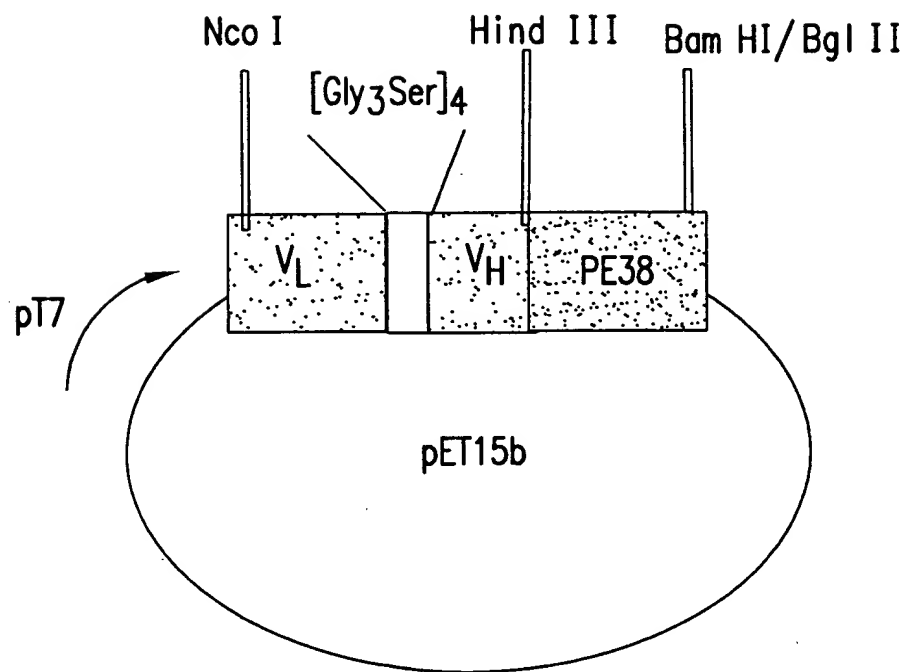


FIG.2

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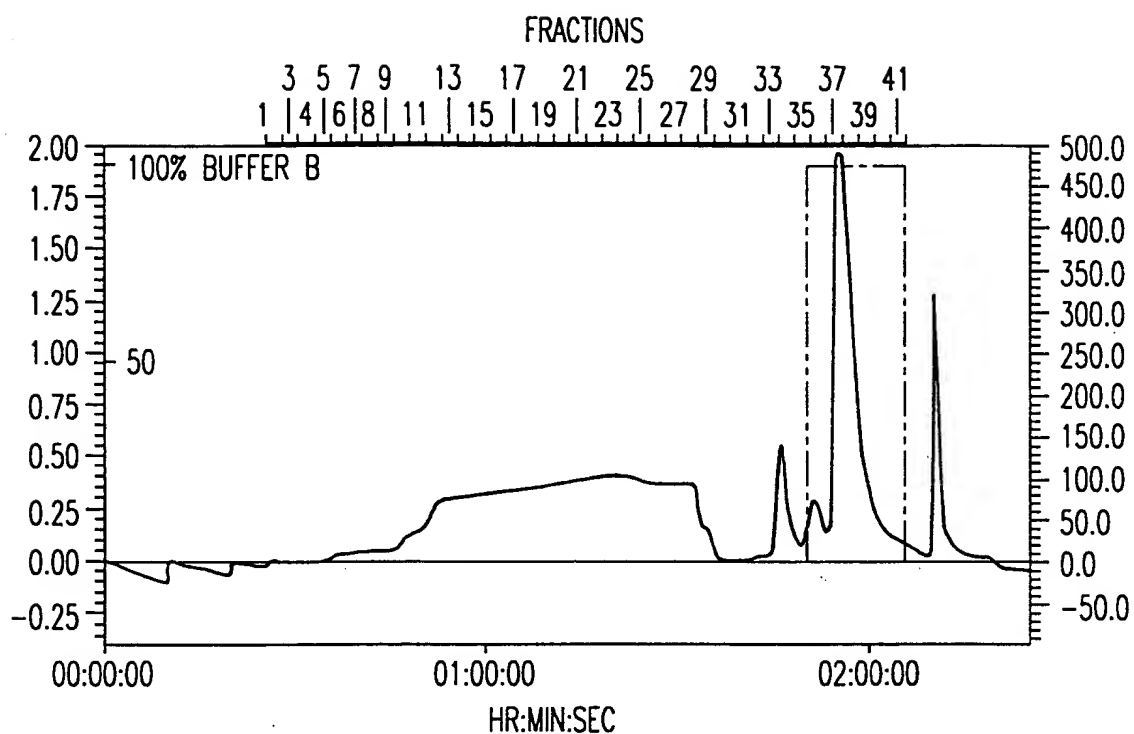


FIG. 3A

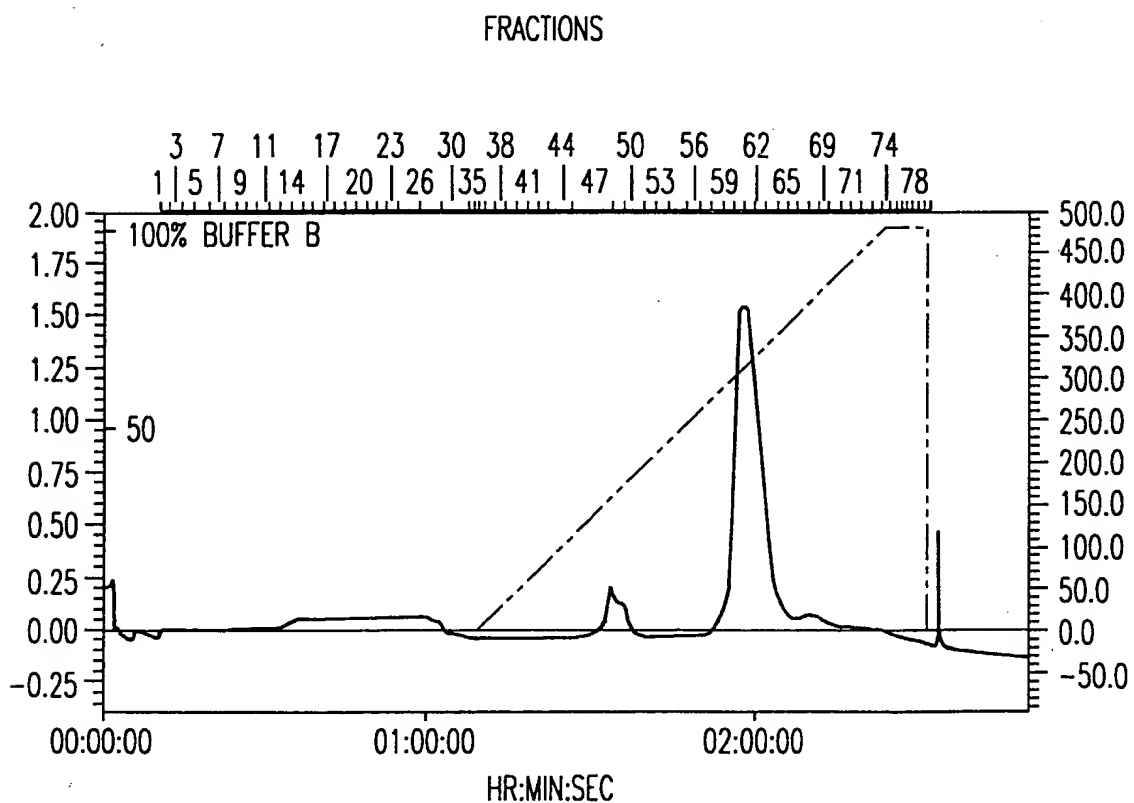


FIG. 3B

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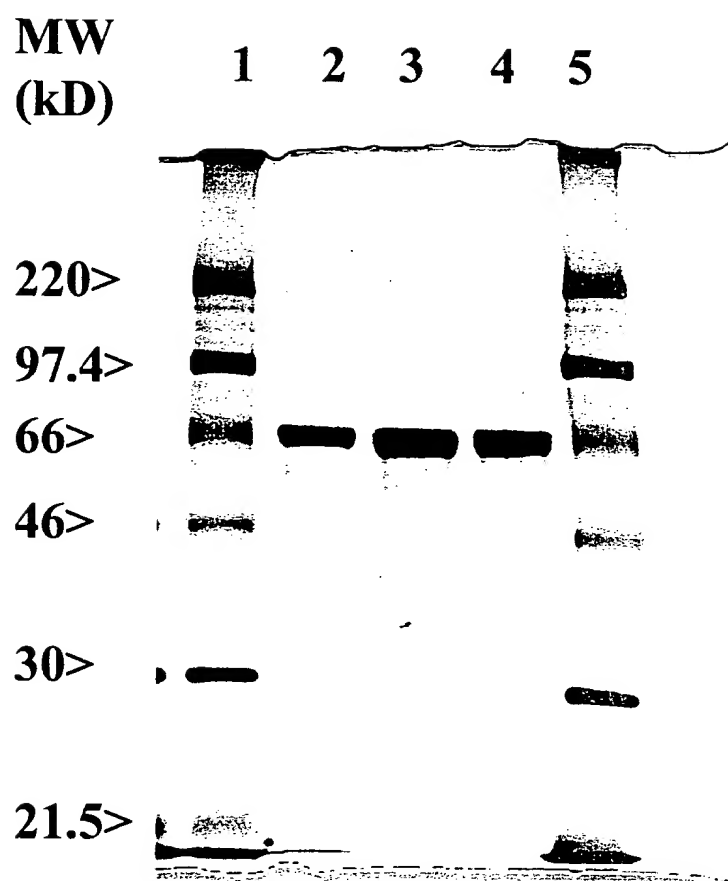


FIG.4

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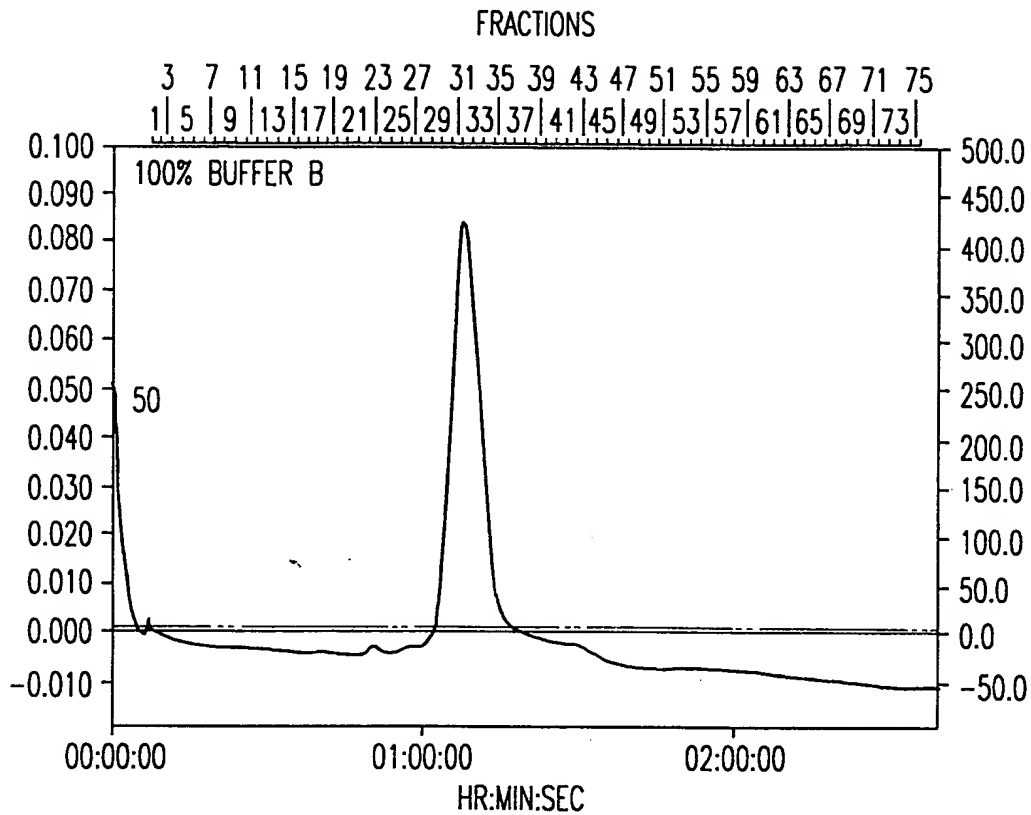


FIG. 5A

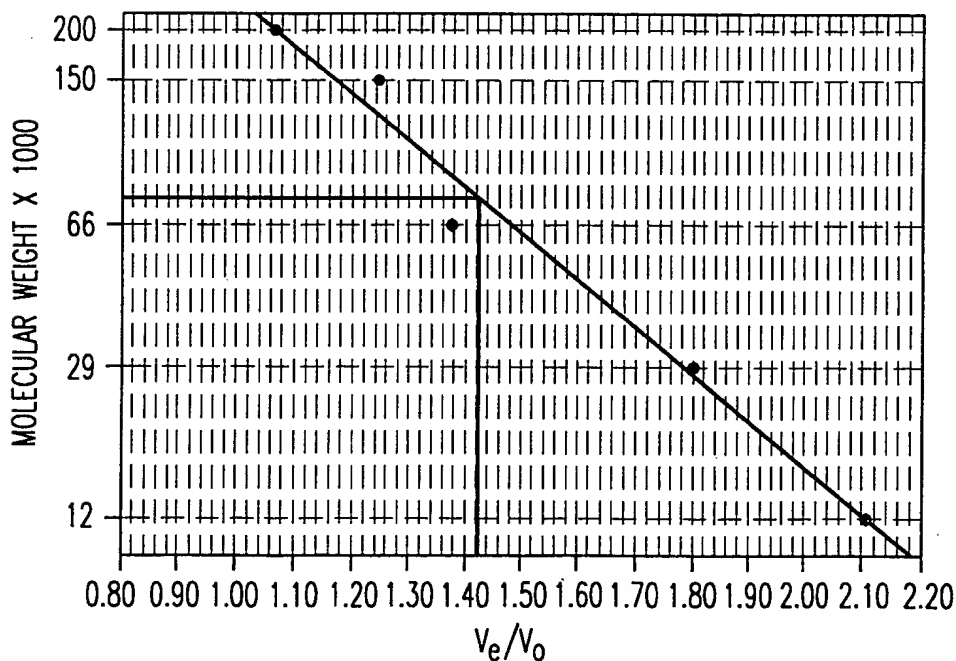


FIG. 5B

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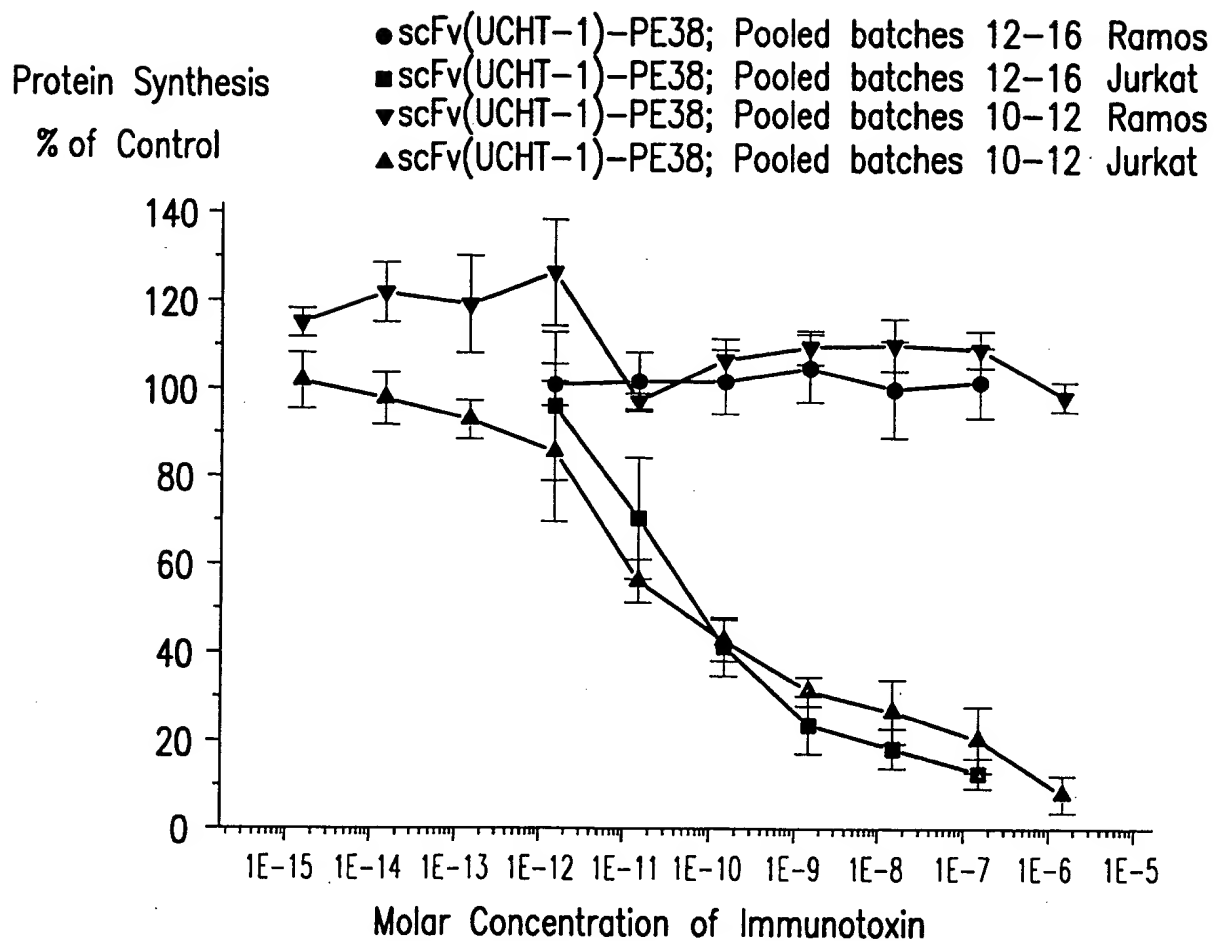


FIG.6

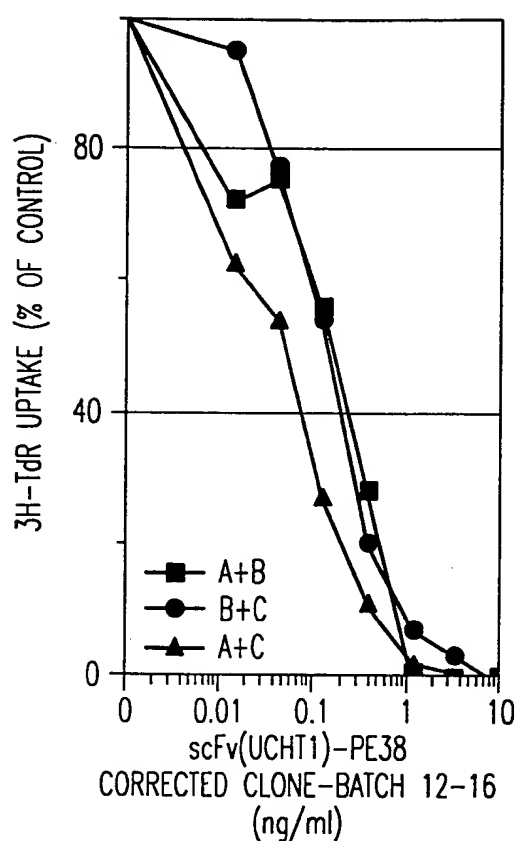


FIG. 7A

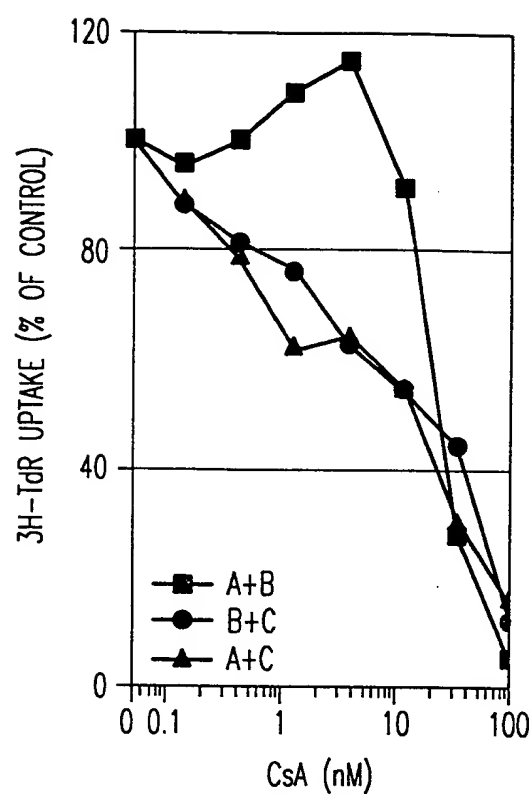


FIG. 7B

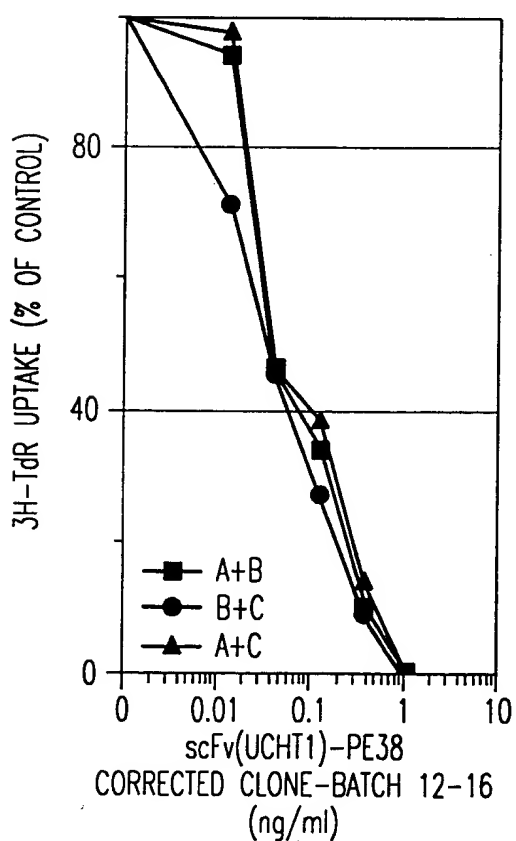


FIG. 7C

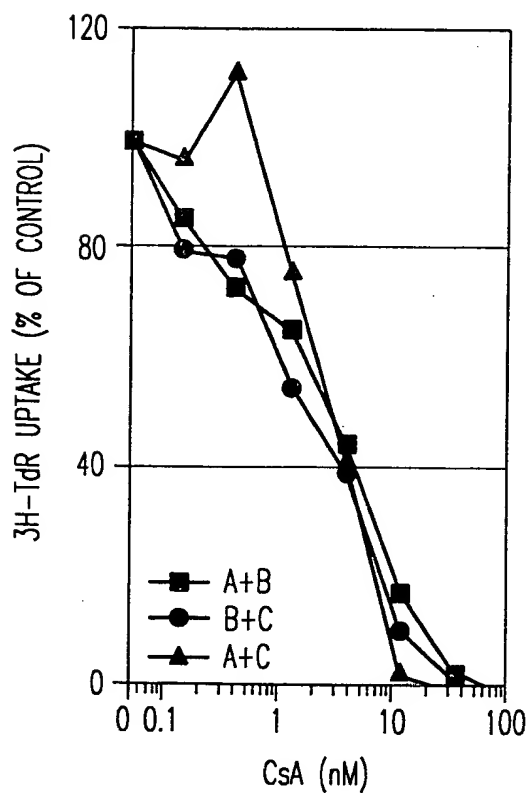


FIG. 7D

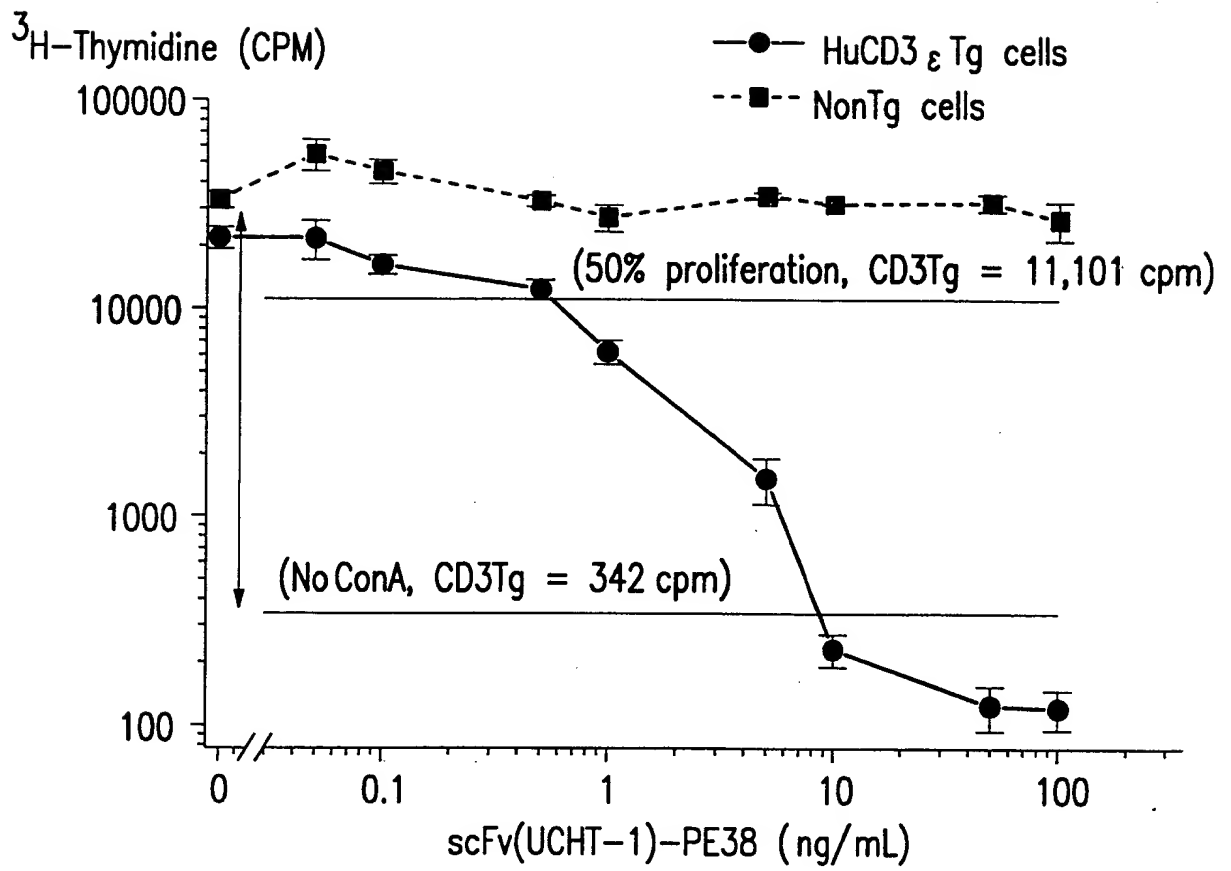


FIG.8

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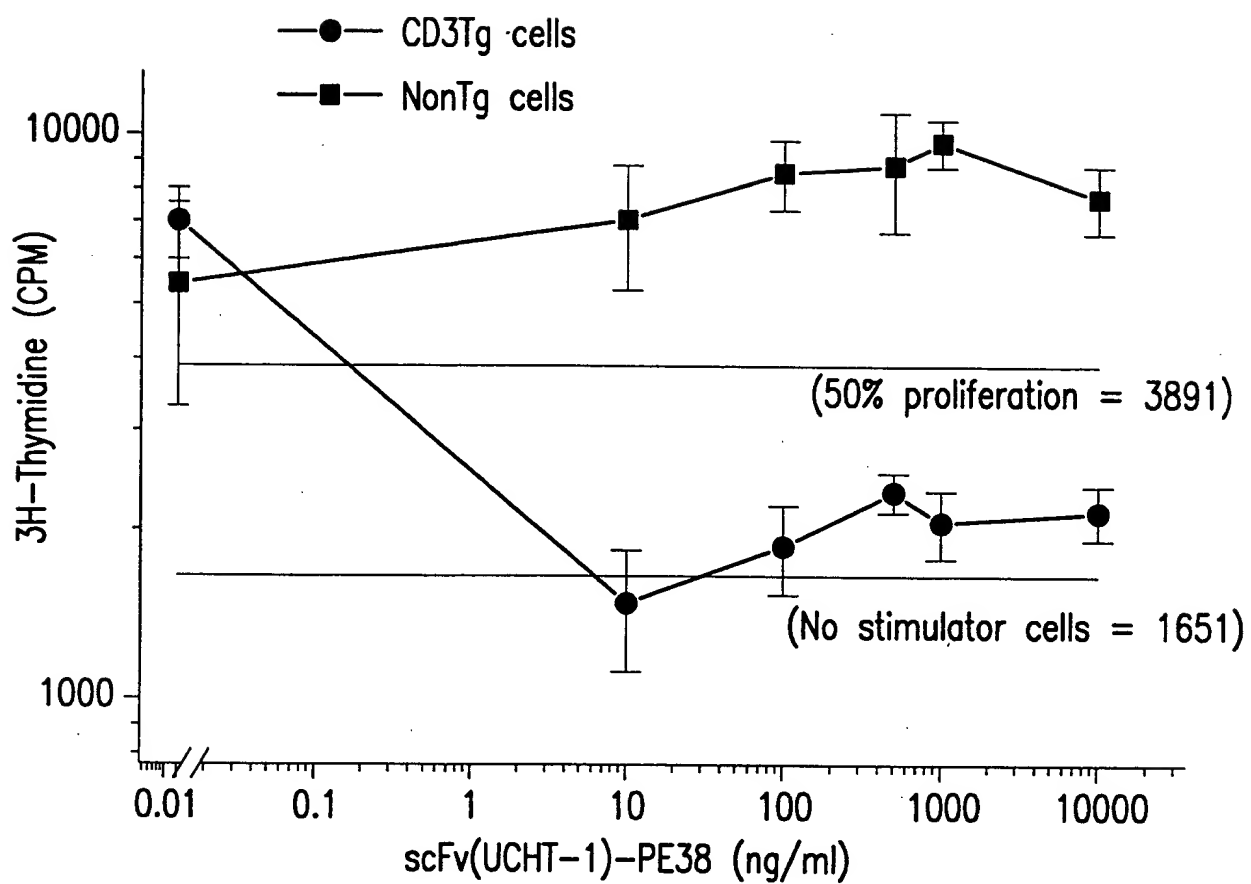


FIG. 9A

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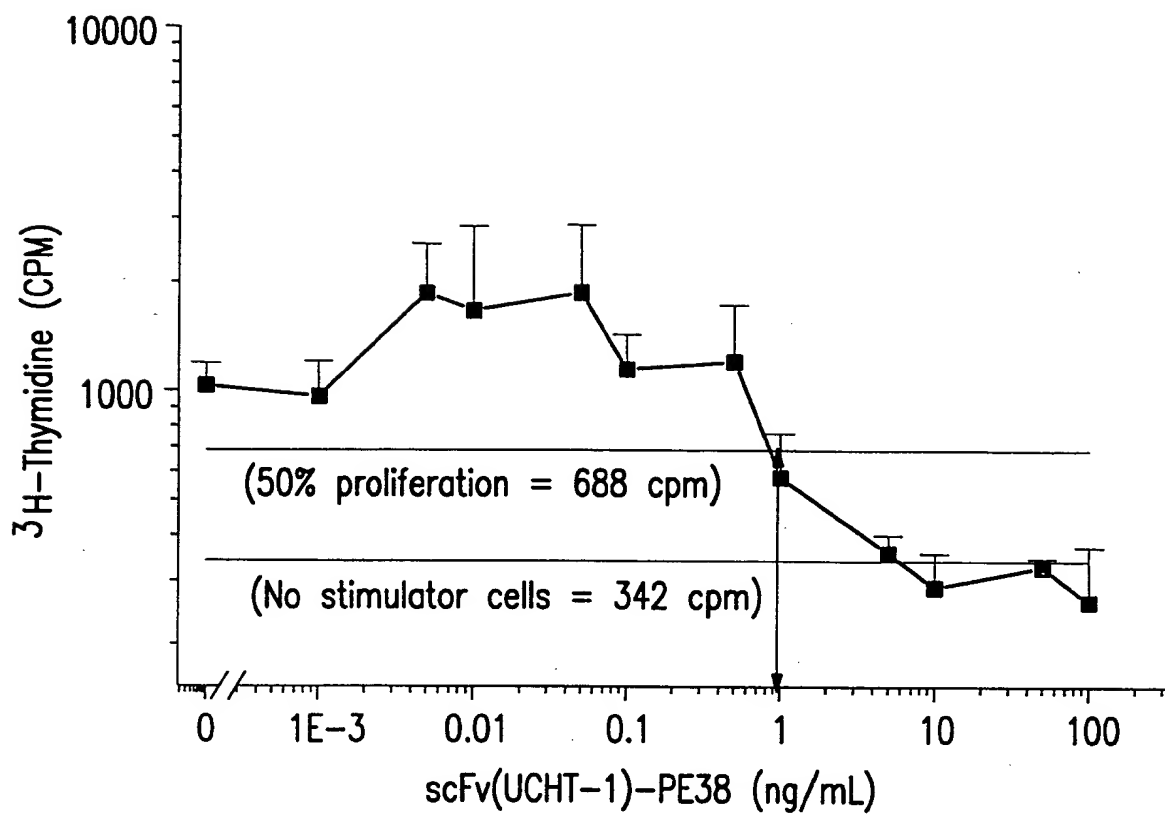


FIG. 9B

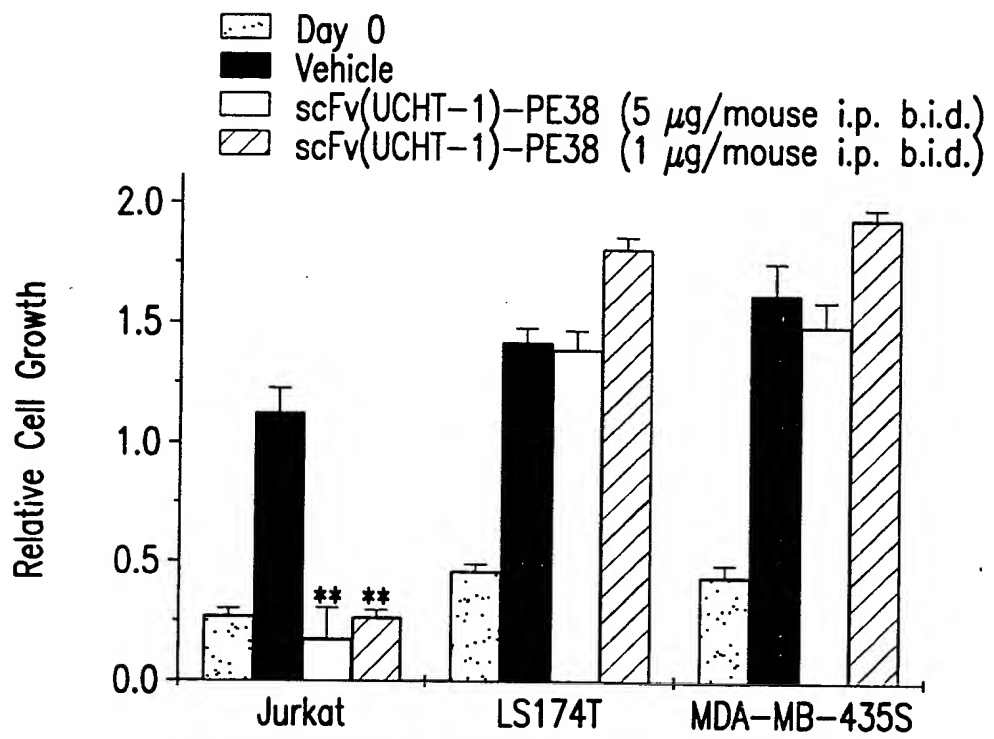


FIG.10

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SPLEEN CELLS

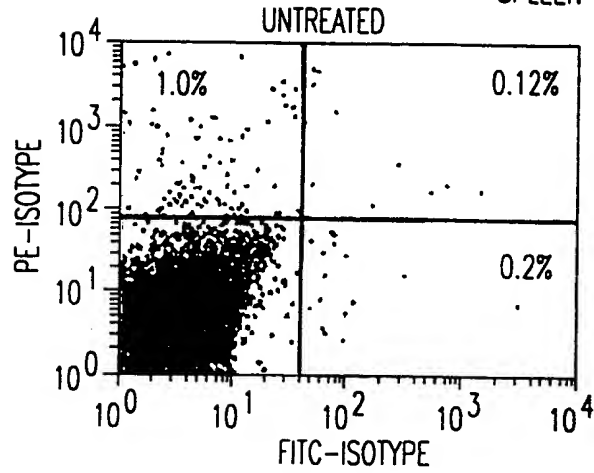


FIG. 11A

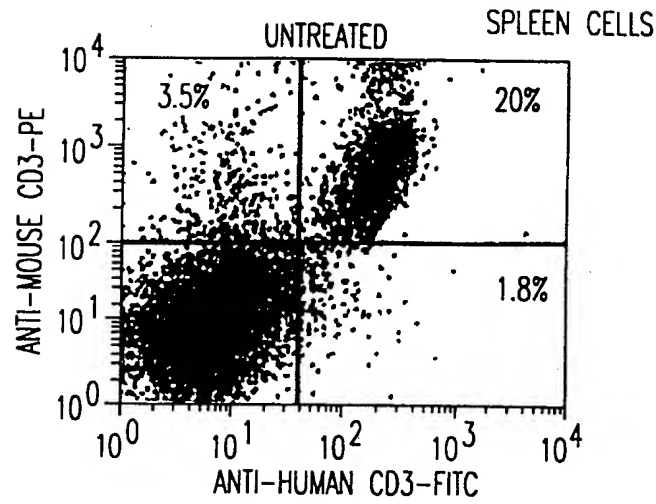


FIG. 11B

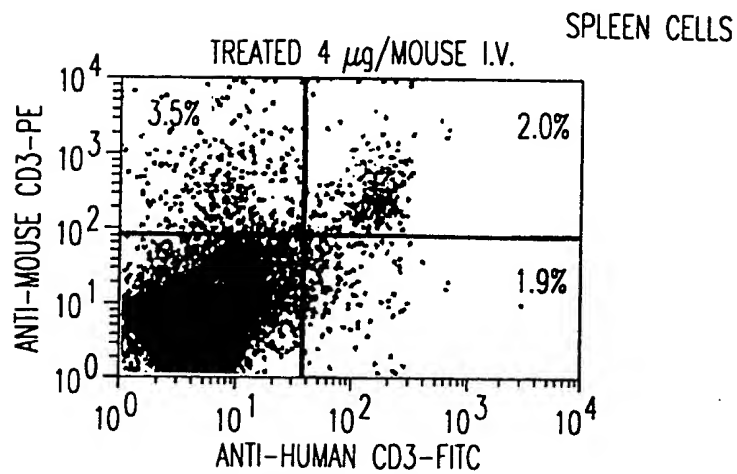


FIG. 11C

00010 8200460

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LYMPH NODE

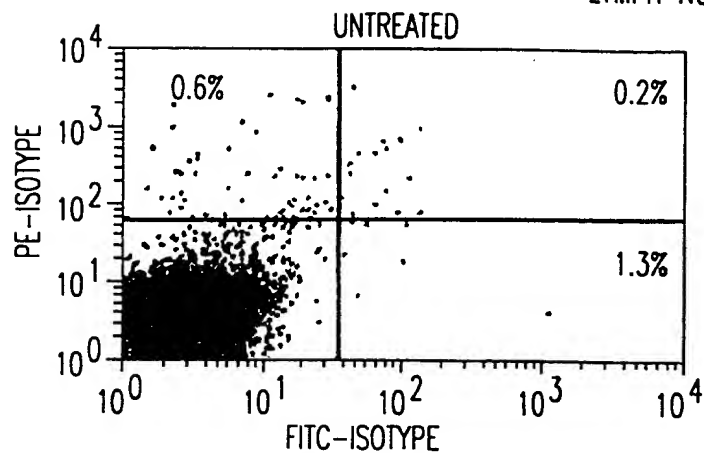


FIG. 12A

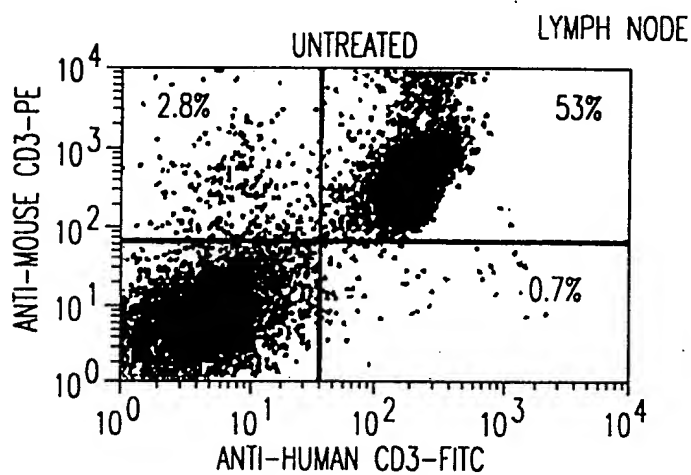


FIG. 12B

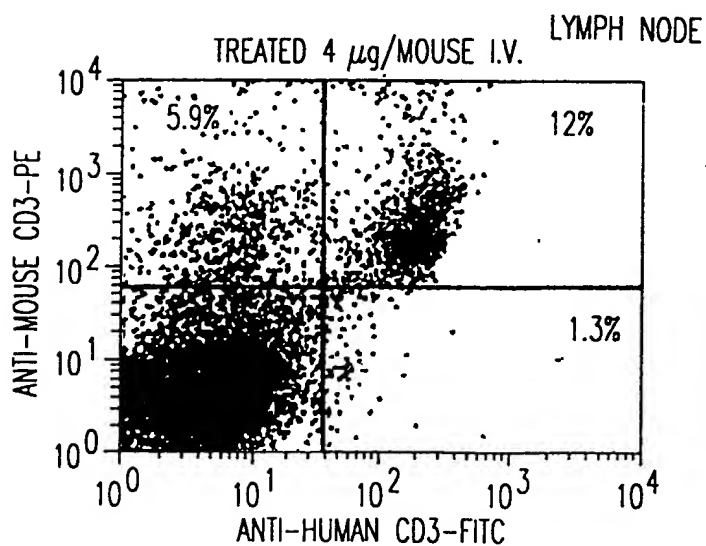


FIG. 12C

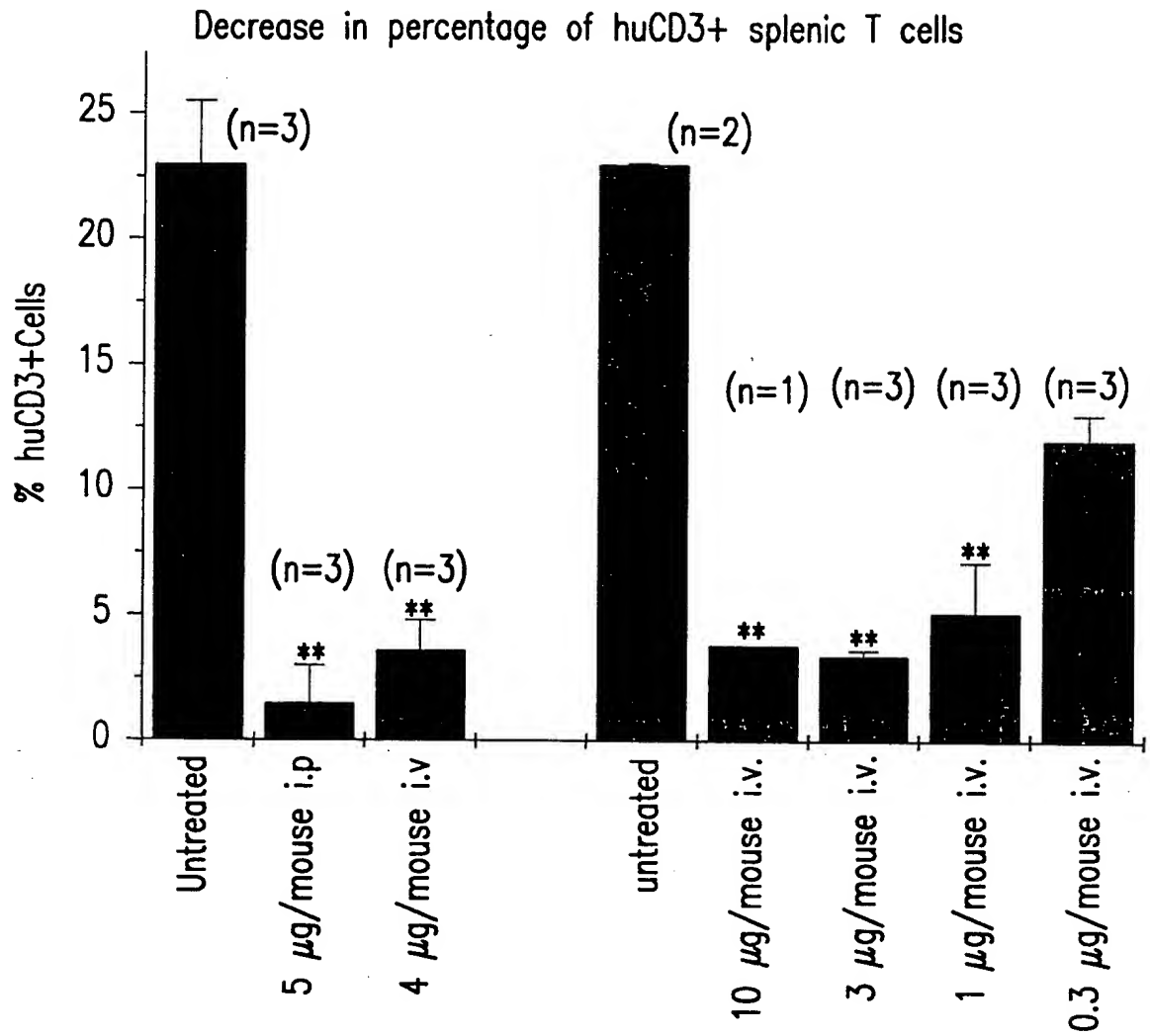


FIG. 13A

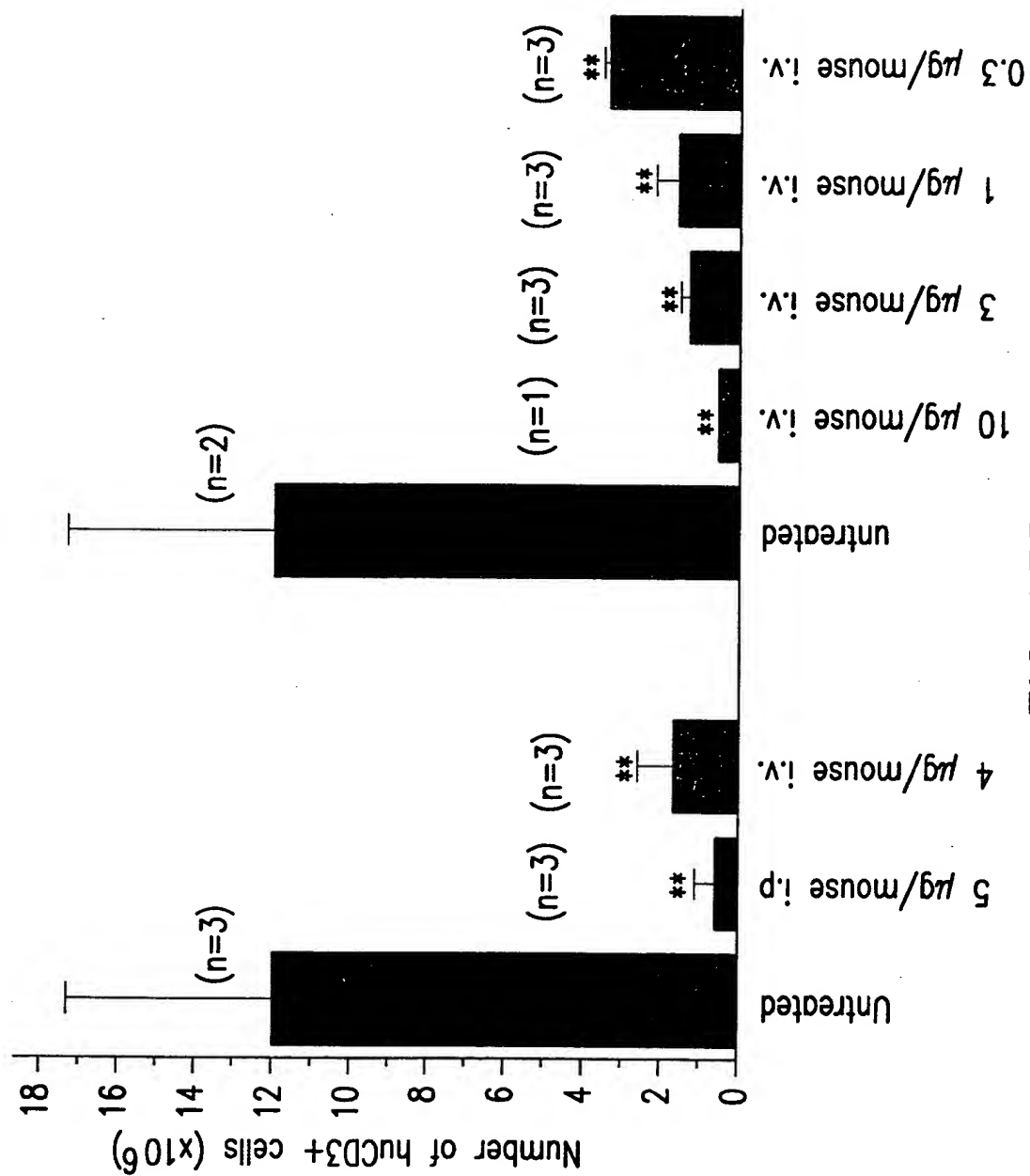


FIG. 13B

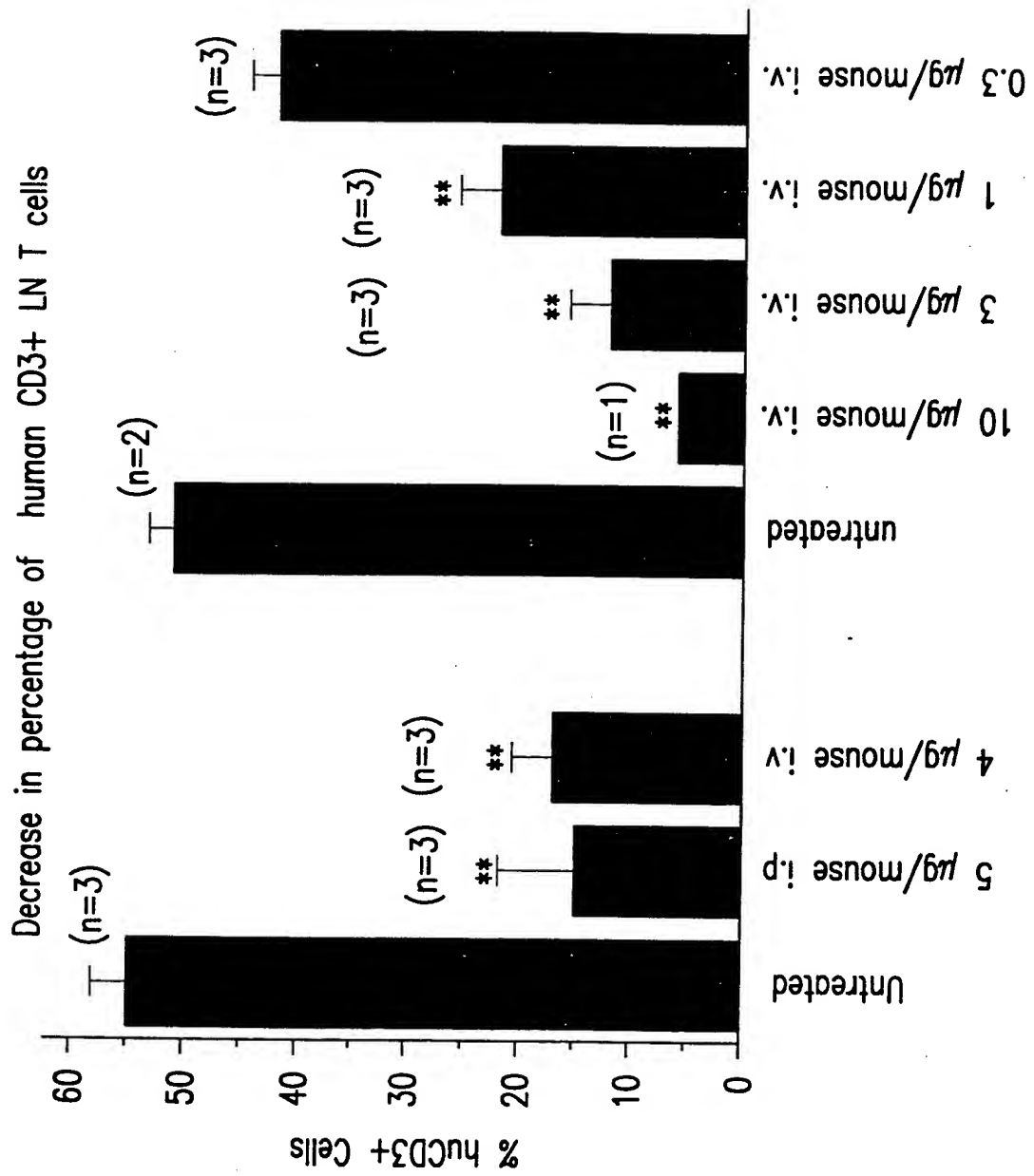


FIG. 14A

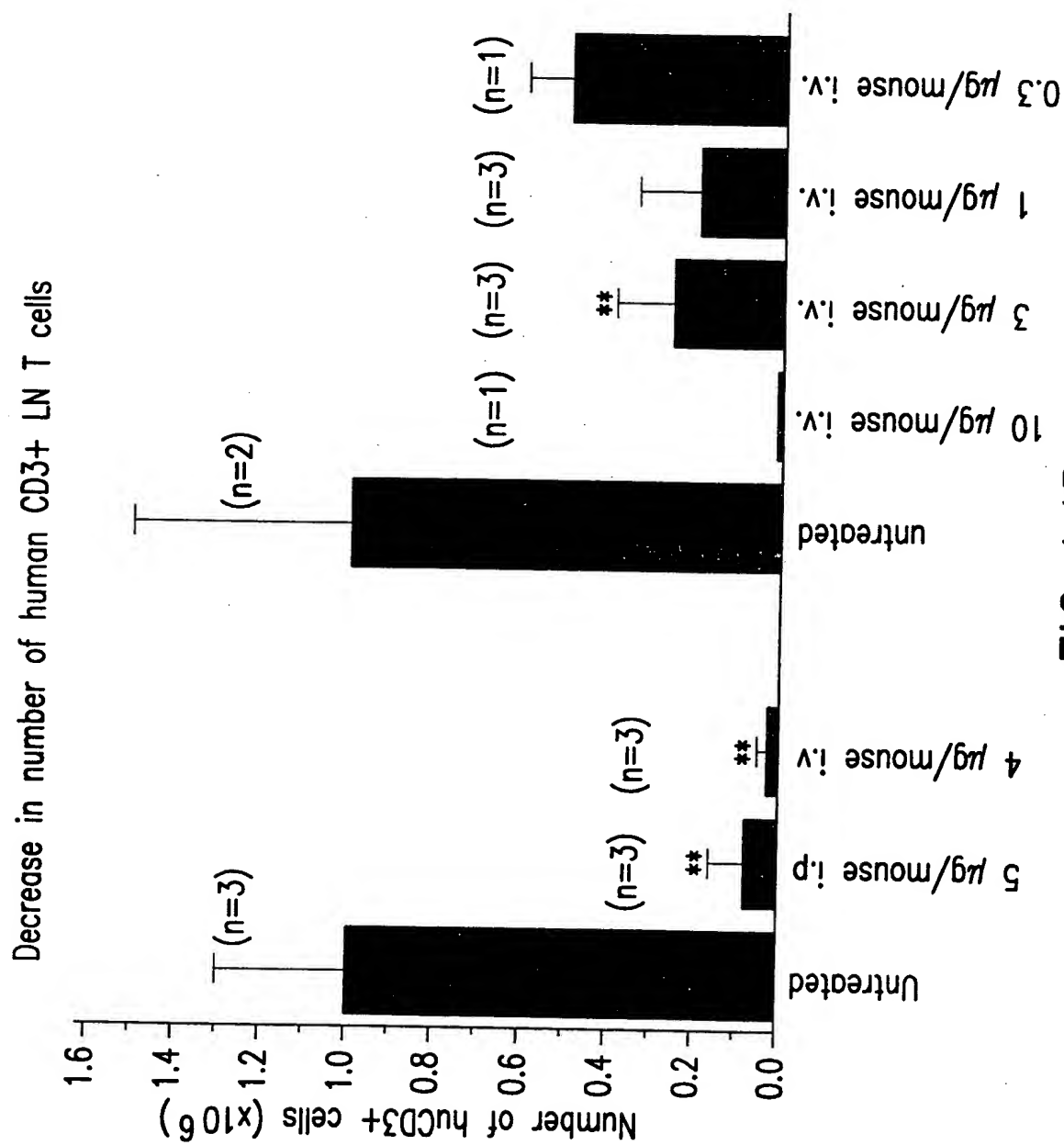


FIG. 14B

Nucleotide and amino acid sequence of scFv(UCHT-1)-PE38

1 CCATGGCGGACATCCAGATGACCCAGACCACCTCCTCCCTGTCTGCCTCTCTGGGAGACA 60
 M A D I Q M T Q T T S S L S A S L G D R
 61 GAGTCACCATCAGTTGCAGGGCAAGTCAGGACATTAGAAATTATTTAAACTGGTATCAAC 120
 V T I S C R A S Q D I R N Y L N W Y Q Q
 121 AGAAACCAGATGGAAGTGTAAACTCCTGATCTACTACACATCAAGATTACACTCAGGAG 180
 K P D G T V K L L I Y Y T S R L H S G V
 181 TCCCATCAAAGTTCAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAGCAACC 240
 P S K F S G S G S G T D Y S L T I S N L
 241 TGGACCAAGAGGATATTGCCACTTACTTTTGCCAACAGGGTAATACGCTTCCGTGGACGT 300
 E Q E D I A T Y F C Q Q G N T L P W T F
 301 TCGCTGGAGGCACCAAGCTGGAAATCAAACGGGCTGGAGGCGGTAGTGGCGGTGGATCGG 360
 A G G T K L E I K R A G G G S G G G S G
 361 GTGGAGGCAGCGGTGGCGGATCTGAGGTGCAGCTCCAGCAGTCTGGACCTGAGCTGGTGA 420
 G G S G G G S E V Q L Q Q S G P E L V K
 421 AGCCTGGAGCTTCAATGAAGATATCCTGCAAGGCTTCTGGTACTCATTCACTGGCTACA 480
 P G A S M K I S C K A S G Y S F T G Y T
 481 CCATGAACTGGGTGAAGCAGAGTCATGGAAGAACCTTGAGTGGATGGGACTTATTAATC 540
 M N W V K Q S H G K N L E W M G L I N P
 541 CTTACAAAGGTGTTAGTACCTACAACCAGAAGTTCAAGGACAAGGCCACATTAAGTGTAG 600
 Y K G V S T Y N Q K F K D K A T L T V D
 601 ACAAGTCATCCAGCACAGCCTACATGGAAGTCTCAGTCTGACATCTGAGGACTCTGCAG 660
 K S S S T A Y M E L L S L T S E D S A V
 661 TCTATTACTGTGCAAGATCGGGTACTACGGTGATAGTACTGGTACTTCGATGTCTGGG 720
 Y Y C A R S G Y Y G D S D W Y F D V W G
 721 GCGCAGGGACACGGTCACCGTCTCCTCAAAAGCTTCCGAGGTCCCGAGGGCGGCAGCC 780
 A G T T V T V S S K A S G G P E G G S L
 781 TGGCCGCGCTGACCGCGCACCAGGCTTGCCACCTGCCGCTGGAGACTTTCACCGTCATC 840
 A A L T A H Q A C H L P L E T F T R H R

FIG. 15A

841 GCCAGCCGCGCGCTGGAACAACTGGAGCAGTGGCGCTATCCGGTGCAGCGGCTGGTCG 900
 Q P R G W E Q L E Q C G Y P V Q R L V A
 901 CCCTCTACCTGGCGGCGCGCTGTCTGGAACCAGGTGACCAGGTGATCCGCAACGCCC 960
 L Y L A A R L S W N Q V D Q V I R N A L
 961 TGGCCAGCCCCGGCAGCGGCGGCGACCTGGGCGAAGCGATCCGCGAGCAGCCGAGCAGG 1020
 A S P G S G G D L G E A I R E Q P E Q A
 1021 CCCGTCTGGCCCTGACCCTGGCCGCGCGGAGAGCGAGCGCTTCGTCCGGCAGGGCACCG 1080
 R L A L T L A A A E S E R F V R Q G T G
 1081 GCAACGACGAGGCCGCGCGGCCAACGCCCCGGCGACAGCGCGACGCCCTGCTGGAGC 1140
 N D E A G A A N G P A D S G D A L L E R
 1141 GCAACTATCCCACTGGCGCGGAGTTCCTCGGCGACGGCGCGACGTCAGCTTCAGCACCC 1200
 N Y P T G A E F L G D G G D V S F S T R
 1201 GCGGCACGCAGAACTGGACGGTGGAGCGGCTGCTCCAGGCGCACCGCCAACCTGGAGGAGC 1260
 G T Q N W T V E R L L Q A H R Q L E E R
 1261 GCGGCTATGTGTTCTGCTCGGCTACCACGGCACCTTCCTCGAAGCGGCGCAAAGCATGCTCT 1320
 G Y V F V G Y H G T F L E A A Q S I V F
 1321 TCGCGGGGTGCGCGCGCGCAGCCAGGACCTCGACGCGATCTGGCGGGTTTCTATATCG 1380
 G G V R A R S Q D L D A I W R G F Y I A
 1381 CCGGCGATCCGGCGCTGGCCTACGGCTACGCCAGGACCAGGAACCCGACGCACGCGGCC 1440
 G D P A L A Y G Y A Q D Q E P D A R G R
 1441 GGATCCGCAACGGTGGCCTGCTGCGGTCTATGTGCCGCGCTCGAGCCTGCCGGGCTTCT 1500
 I R N G A L L R V Y V P R S S L P G F Y
 1501 ACCGCACCAGCCTGACCCTGGCCGCGCGGAGGCGGGGCGAGGTGCAACGGCTGATCG 1560
 R T S L T L A A P E A A G E V E R L I G
 1561 GCCATCCGCTGCCGCTGCGCCTGGACGCCATCACCGCCCCGAGGAGGAAGCGGGCGGCC 1620
 H P L P L R L D A I T G P E E E G G R L
 1621 TGGAGACCATTCTCGGCTGGCCGCTGGCCGAGCGCACCGTGATTCCCTCGGCGATCC 1680
 E T I L G W P L A E R T V V I P S A I P

FIG. 15B

1681 CCACCGACCCGCGCAACGTCGGCGGCGACCTCGACCCGTCCAGCATCCCCGACAAGGAAC 1740
T D P R N V G G D L D P S S I P D K E Q

1741 AGGCGATCAGCGCCCTGCCGGA CTACGCCAGCCAGCCCGCAAACCGCCGCGGAGGACC 1800
A I S A L P D Y A S Q P G K P P R E D L

1801 TGAAGTAACTGCCGCGACCGCGCGGCTCCCTTCGCAGGAGCCGGCCTTCTCGGGGCCTGG 1860
K *

1861 CCATACATCAGGTTTTCTGATGCCAGCCCAATCGAATATGAATTCCTCGAGACGTACGG 1920

1921 TCGCGCGGATGCATTGAAGATCC 1944

FIG. 15C

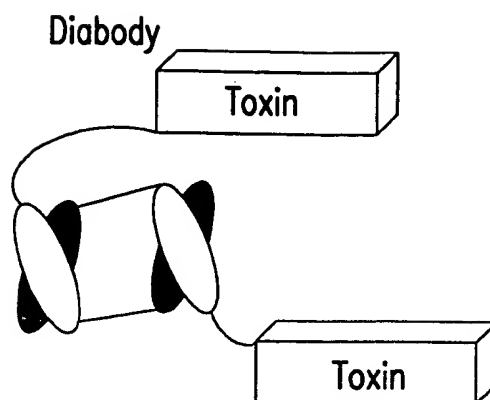


FIG. 16A

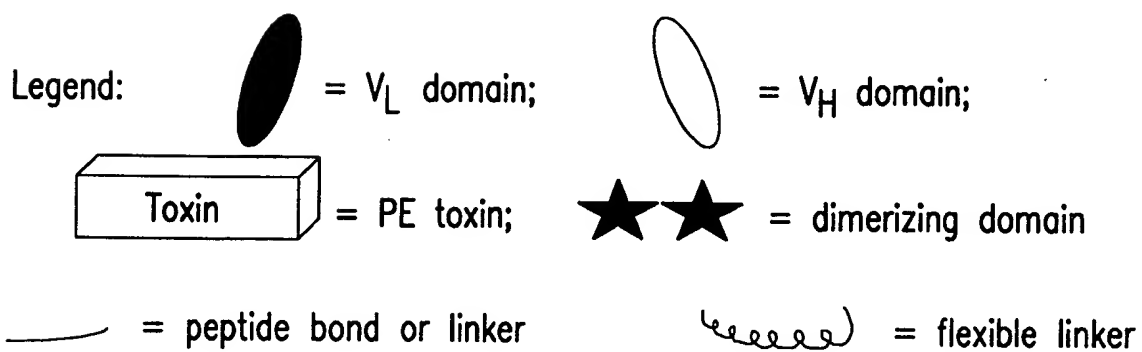
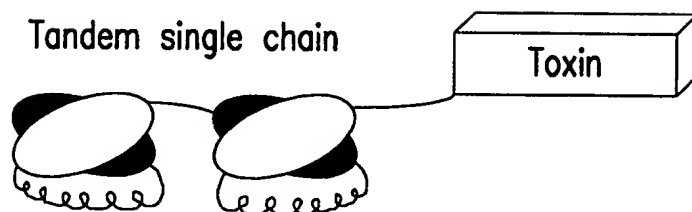


FIG. 16B

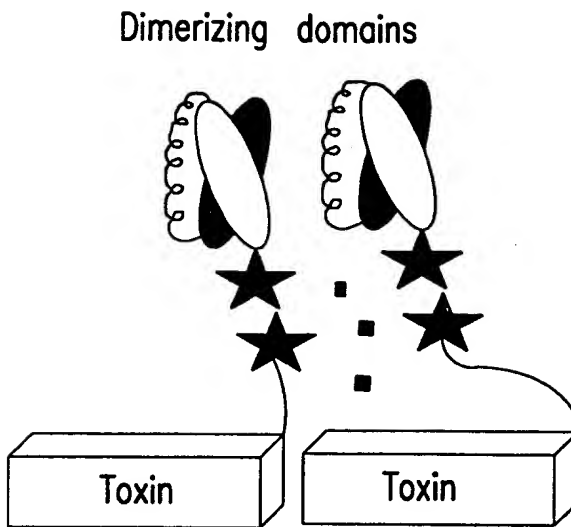


FIG. 16C

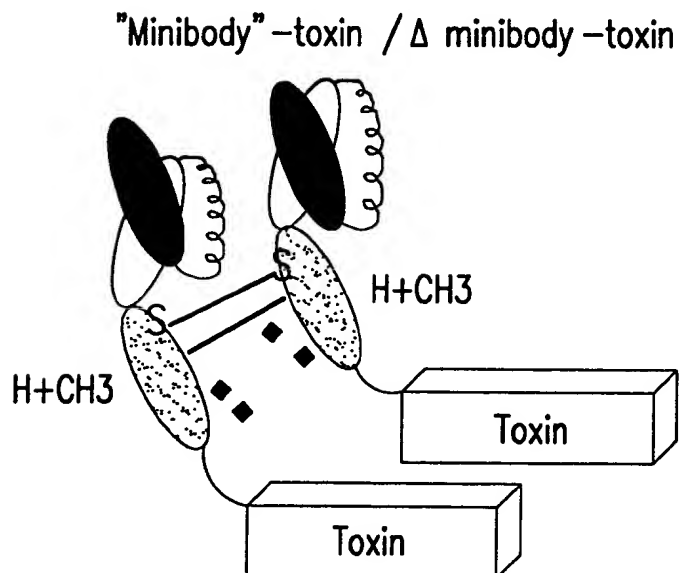


FIG. 16D

